Post-processing: Minimum Match 0% Maximum Match 100% L1sting first 45 summaries Title: Perfect score: Database : Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Total number of hits satisfying chosen parameters: Scoring table: Sequence: Run on: OM nucleic - nucleic search, using sw model IDENTITY\_NUC
Gapop 10.0 , Gapext 1.0 November 29, 2001, 04:04:14; Search time 6128:19 Seconds (without alignments) 2020.032 Million cell updates/sec US-09-526-329-38 1152 11351937 seqs, 5372889281 residues GenCore version 4.5 Copyr1ght (c) 1993 - 2000 Compugen Ltd. em\_htc:\*
gb\_est1:\*
gb\_est2:\*
gb\_htc:\*
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gb\_htc:\*
em\_gss\_hum:\*
em\_gss\_inv:\*
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em\_gss\_other:\* em\_estin:\*
em\_estom:\* em\_estba:\* em\_estov:\* em\_estfun:\* em\_estro:\* em\_estpl:\* em\_esthum:\* 22703874

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	6000	Query	2	á	:	
No.	Score	Match	Length DB	. ₩	ID	Description
c 1	664.4	57.7	674	10	AW978572	AW978572
c 2	606.6	52.7	657	10	AW370369	AW370369
c 3	498.2	43.2	508	10	AA825207	
c 4	493	42.8	495	10	AW575965	AW575965 UI-HF-BL
c 5	454.4	39.4	456	10	AI379831	AI379831
c 6	407	35.3	407	10	AI224367	
c 7	396.4	34.4	398	10	AW292092	
က 8	374.4	32.5	376	10	A1832007	
c 9	372.8	32.4	525	10	AI250843	AI250843 qx10a04.x
10	349.4	30.3	358	10	AW404913	
c 11	331.4	28.8	338	10	AA825205	0,
c 12	312.8	27.2	328	10	AW003249	AW003249

4.	4.	4	4.	4	41	ω	<u>پ</u>	ω	3	ω	ω	ω	ω	ω	ω	2	2	2	2	2	2	c 2:	2:	c 21	2	11	브	1	c 1	11	c 1	
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578	576	574	570	566	559	554	554	553	547	535	515	511	494	494	493	449	431	537	365	472	282	161	148	178	457	560	389	463	265	492	300	315
11	10	10	1	10	H	11	11	10	10	10	10	10	10	10	10	11	10	10	10	11	10	11	10	10	13	10	10	13	10	13	10	10
BG759756	2803	W73266	BI226934	BE295457	126135	BI225862	BI225045	BE513898	BE269500	BE268990	BE267967	BE398017	AW732980	AW500764	BE267581	BF128815	AW405686	AI391250	AW014278		AW345961	BF082894	AA689513	AI468861	AQ518451	BE685287	AW480639	AQ572549	AW768336	AQ589625	AI250350	AI434322
BG759756 602711155	AW328037 dr03q06.x	AW732667 bb10h10.y	BI226934 602952063	BE295457 601174505	BI261356 602953358	BI225862 602950239	BI225045 602949269	BE513898 601316486	BE269500 601184704	BE268990 601184424	BE267967 601125372	BE398017 601290574	AW732980 bb18d04.y	AW500764 UI-HF-BN0	BE267581 601124363	BF128815 601811195	AW405686 UI-HF-BLO	AI391250 mb58c01.y	UI-H-B	272392	26836 MA	QV1-BT08	AA689513 ns17q04.r	AI468861 ti43b01.x	AQ518451 HS_5101_A	BE685287 187456 MA	AW480639 32244 MAR	AQ572549 HS_2137_B	hk72q05	AQ589625 HS_2132_A	AI250350 qx04c01.x	ti41d01

## ALIGNMENTS

185 a	y/12 medical center Dr., kockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: johngetigr.org Plate: 394 Plate: 394 Seq primer: Forward. FEATURES Location/Qualifiers Source 1.674	Quackenbush, J.  Quackenbush, J.  Quackenbush, J.  Quackenbush, J.  Quackenbush, J.  Quackenbush Gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray  JOURNAL Unpublished (2000)  COMMENT Contact: John Quackenbush  The Institute for Genomic Research	KEYWORDS EST.  SOURCE human:  ORGANISM Homo sapiens  ORGANISM Homo sapiens  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE 1 (bases 1 to 674)  AUTHORS Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt  AUTHORS J. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and	RESULT 1 AW978572/C AW978572 674 bp mRNA DDETINITION E5T390681 MAGE resequences, MAGF ACCESSION AW978572.1 GI:8169840 VERSION AW978572.1 GI:8169840
MAGP"	20850, USA	in a model of colon tumor microarray	Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo. ernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt Sharov,V., Lee,N.H., Yeatman,T.J. and	674 bp mRNA EST 02-JUN-2000 MAGE resequences, MAGP Homo sapiens cDNA, mRNA sequence. 1 GI:8169840

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RESULT 2
AW370369/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1113 ttattgctcactgt 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 TTGCACAGTGGGGAGCATGGAGGGATGGGTTTGGCCTGCTTCTGCTTATTCAGTCCTT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          993 ctgcacagtgggggatggaatggagtttgggcttgtgcttctgcttattcagtcctt 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 AGCTCGTGATTGGAAACTCACCATCGGCAGGCAGTGGTTCGGTTTAAGAGATGGCATTAC 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   494 TGGCCTGGATGGGCTTCACTGGGGCCCTGTCTGTGTGCTGAGCCAGTTTCCCCTGCTGCC 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      633 tggcctggatgggcttcactggggccctgtctgtgtgctgagccagtttccccttgctggc 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        573 tctcgttttccttagttatcagtcctgtcctgtcccactcaggtctgtacttagggcagc 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        614 CACACCCAGCATAGCCTCCTTGCAGGCAGAAGGCAGTAGGGCCCCTGCACACTCAGTTTC 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      674 GGGCTGGTGTCTCCTCATGCCCCCTCAGTGAGGATCTTCATGTACCTGTTCTTCTTGTTTG 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       453 ggcctggtgtctcctcatgccccctcagtgaggatcttcatgtacctgctcttctgtttg 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         554 TCTCGTTTTCCTTAGTTATCAGTCCTGTCCTGTCCCACTCAGGTCTGTACTTAGGGCAGC 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Loca 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGCCCGAAATAGATCCAGTGCTGAGCAAGCAATGTACACCGGAGCCTCAGTGAGCCCAT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agggageccagtctggatgtggacttggatgccctgtggggtatcagttctgctgacactt 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tgcaagctgtgggttctttctcctctgtgcccctcatgctgatcttctagatgccactcc 752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGGAGCCCAGTCTGGATGTGGACTTGGATGCCCTGTGGGTATCAGTTCTGCTGACACTT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agctcgtgattggaaactcaccatcggcaggcagtggttcggtttaagagatggcattag 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCAAGCTGTGGGTTCTTTCTTCTGTGCCCCTCATGCTGATCTTCTAGATGCCACTCC
                                                                                                                                    HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt AW370369} \\ 657 \ {\tt bp} \\ {\tt mRNA} \\ EST \\ 04-{\tt FEB-2000} \\ {\tt RC1-BT0255-181099-012-f04} \\ {\tt BT0255} \ {\tt Homo} \ {\tt sapiens} \ {\tt cDNA}, \ {\tt mRNA} \ {\tt sequence}.
                        Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                               Contact: Simpson A.J.G
                                                                                                                                                                                                                                                                                                                                               EST
                                                                                                                                                                                                                                                                                                                                                                                                   AW370369
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                       AW370369.1 GI:6875023
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                                                                                                                                                                                                                          Eutheria; Primates; Catarrhini; Hominidae; Homo
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99.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 664.4; DB 10; Length Pred. No. 1.1e-111; O; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 674;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
1085 tgacctcacagtactggttaattaaactttattgctc 1121
                                                                                  1025 ggcctgtgcttctgcttattcagtccttcagctcacggaagggatgctagtccgtgaagg 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                    965 atgtacaccggagcctcagtgagcccatctgcacagtggggagcatggagggatgggttt 1024
                                                                                                                                                                                                                                                                                       237
                                                                                                                                                                                                                                                                                                                                                                                                   297 AGTGGTTCGGTTTAAGAGATGGCATTAGAGGGAGCCCAGTCTGGATGTGGACTTGGATGC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 CTCATGCTGATCTTCTAGATGCCACTCCCAAATCCCCCTTCATACCCCACCAGGATGTGTGC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    537 TCCCACTCAGGTCTGTACTTAGGGCAGCTGGCCTGGATGGGCCTTCACTGGGGCCCTGTCT 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      605 tcccactcaggtctgtacttagggcagctggcctggatgggcttcactgggggccctgtct 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      597 GCAGTAGGGCCCCTGCACACTCAGTTTCTCTCGTTTTCCTTAGTTATCAGTCCTGTCCTG 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      485 gatetteatgtacetgetettetgtttgcacacecagcatagcetecttgcaggcagaag 544
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                                                                                                                                                                                                                                                                                                                   agtggttcggtttaagagatggcattagagggagcccagtctggatgtggacttggatgc 904
                                                       GGCCTGTGCTTCTGCTTATTCAGTCCTTCAGCTCACGGAAGGGATGCTAGTCCGTGAAGT 58
                                                                                                                                                                     ATGTACACCAGAGCCTCAGTGAGCCCATCTGCACAGTGGGGAGCATGGAGGGATGGGTTT 118
                                                                                                                                                                                                                                                                                 ccagccaggcctccagcacccccagtgcagctcgtgattggaaactcaccatcggcaggc 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ctcatgctgatcttctagatgccactcccaaatccccttcatacccaccaggatgtgtgc 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gcagtagggcccctgcacactcagtttctctcgttttccttagttatcagtcctgtcctg 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence start: 29 High quality sequence stop: 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1&t2=RC1-BT0255-181099-012-f04&t3=1999-10-18&t4=1)
Seq_primer: puc_18_forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brazil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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174 c 187 g 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_l1b="BT0255"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.7%; Score 606.6; DB 10; 97.0%; Pred. No. 3.9e-101;
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Indels Length 657;

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57 GACCTCACAGTACCTGGTTAATTAAACTTTATTGCTC 21

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                                            770 caccaggatgtgtgcccagccaggcctccagcacccccagtgcagctcgtgattggaaac 829
                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                     500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www-blo.llnl.gov/bbrp/image/hmage.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 449.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert Length: 1099 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOMD'T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA825207.1 GI:2898504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 508)
                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pn.D.
                                                                                                                                                                                                                                                                                                                                             constructed by Bento Soares and M. Fatima Bonaldo." a 129 c 132 g 122 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                                                                                                                                                                                                                                                                                                                                                                                     Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization, and was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1354692"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="NCI_CGAP_GCBl"
                                                                                                                                                                                                                                     43.2%;
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 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       830 tcaccatcggcaggcagtggttcggtttaagagatggcattagagggagcccagtctgga 889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 AAAAAAAAAAAAAAAAAAAA 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M.B. Soares Lab cDNA Library Preparation: M.B. Soares Lab cDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PULYA=Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 495)
/lab_host="pB108 (LTI)"
/note="Vector: pT773-Pac; Site_1: Not1; Site_2: Eco RI;
/note="Vector: pT773-Pac; Site_1: Not1; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt., ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3059932"
                                                                                                                                                                                   /cell_type="germinal center B cells"
/cell_line="MGC85"
                                                                                                                                                                                                                                          /clone_lib="NIH_MGC_37"
/tissue_type="lymph"
                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 746 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                               EST
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                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                      Unpublished (1997)
                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                AI379831.1 GI:4189684
                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                (bases 1 to 456)
                                                                                                   primer: -40UP from Gibco
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                                                                              quality sequence stop: 455.
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  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.8%;
99.6%;
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    Mismatches

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                                                                            REFERENCE
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  JOURNAL
                                        TITLE
                                                           AUTHORS
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qx05f07.x1 NCI_CGAP_Lym12
Unpublished (1997)
                                                                                                                                                                                                                   mRNA sequence.
AI224367
                       Tomor.
                                                                                                                                       Homo sapiens
                                                                                                                                                                                              AI224367.1 GI:3807080
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                       Gene Index
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99.8%;
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1035 tetgettatteagteetteageteaeggaagggatgetagteegtgaaggtgaecteaea 1094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 GAGCCTCAGTGAGCCCATCTGCACAGTGGGGAGCATGGAGGGATGGGTTTTGGCCTGTGCT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 TTTAAGAGATGGCATTAGAGGGAGCCCAGTCTGGATGTGGACTTGGATGCCCTGTGGGTA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          855 tttaagagatggcattagagggagcccagtctggatgtggacttggatgccctgtgggta 914
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homol1 (bases 1 to 407)
                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a modified polylinker; Site_1: Not I; Site_2: Ecc RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_CCBl) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified coNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-392087, 682632-687239,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. " a 120 c 125 g 94 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
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/clone_lib="Soares_NFL_T_GBC_S1"
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                                                                                                                                                                                                                                                                                                                                                                           RNA EST 21-DEC-1998 Homo sapiens cDNA clone IMAGE:2000485 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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                                          TITLE
                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                           1085 tgacctcacagtactggttaattaaactttattgctcactgtcaaaa 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    965 atgtacaccggagcctcagtgagcccatctgcacagtgggggagcatggagggatgggttt 1024
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                                                                                                                                                                                                                                                                                                                                                                      47 TGACCTCACAGTACTGGTTAATTAAACTTTATTGCTCACTGTCAAAA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW292092 398 bp mRNA EST 16-JAN-2000 UI-H-BIZ-agx-a-12-0-UI-B NCI_CGAP_SUb4 Homo sapiens cDNA clone IMAGE:2725559 3', mRNA sequence.
Unpublished (1997)
                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                EST
                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 398)
                                                                                                                                        Homo sapiens
                                                                                                                                                                                               AW292092.1 GI:6698728
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unknown library type
Insert Length: 675 Std Err
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"

a 109 c 107 g 91 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE: 2000485"
/clone_lib="NCI_CGAP_Lym12"
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+ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.3%; Score 407; DB 10; Length 407; 100.0%; Pred. No. 1.1e-64;
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867 cattagagggagcccagtctggatgtggacttggatgccctgtgggtatcagttctgctg 926
                                                                                                                                                807 cagrgcagctcgtgattggaaactcaccatcggcaggcagtggttcggtttaagagatgg 866
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                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                       397;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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//lab_inst="millo (Life Technologies)"
//note="vector: pr773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NCI_CGAP_Sub4 library is a subtracted library derived from
the NCI_CGAP_Sub2 library which is a subtracted library
derived from the NCI_CGAP_Sub1 library, which is a
subtracted library derived from BI. BI constitutes a
mixture of 21 normalized or subtracted NCI_CGAP
librarise: NCI_CGAP_CO16, NCI_CGAP_Kid5,
NCI_CGAP_CO10, NCI_CGAP_CO16, NCI_CGAP_Kid5,
NCI_CGAP_Lei2, NCI_CGAP_LAD13, NCI_CGAP_CO8, NCI_CGAP_P728,
NCI_CGAP_Lei2, NCI_CGAP_Br2, NCI_CGAP_CO8, NCI_CGAP_CO1,
NCI_CGAP_Lei2, NCI_CGAP_Br3, NCI_CGAP_CO8, NCI_CGAP_CO1,
NCI_CGAP_Lo21, NCI_CGAP_Lo19, NCI_CGAP_CO8, NCI_CGAP_CC1,
NCI_CGAP_Lo21, NCI_CGAP_Lo19, NCI_CGAP_CO8, NCI_CGAP_GC6,
NCI_CGAP_Lo22, NCI_CGAP_Lo19, NCI_CGAP_CO8, NCI_CGAP_GC6,
NCI_CGAP_Lo22, NCI_CGAP_Lo19, NCI_CGAP_CO8, NCI_CGAP_GC6,
NCI_CGAP_Lo23, NCI_CGAP_Lo19, NCI_CGAP_CO8, NCI_CGAP_GC6,
NCI_CGAP_Lo23, NCI_CGAP_Lo19, NCI_CGAP_CO8, NCI_CGAP_GC6,
NCI_CGAP_Lo23, NCI_CGAP_Lo19, NCI_CGAP_CO8, NCI_CGAP_GC6,
NCI_CGAP_Lo19, NCI_CGAP_Lo19, NCI_CGAP_CO8, NCI_CGAP_GC6,
NCI_CGAP_Lo19, NCI_CGAP_Lo19, NCI_CGAP_CO8, NCI_CGAP_GC6,
NCI_CGAP_Kid3 pool 1: LLAM 3334-3337, 3682-3683,
3798-3803 (IMAGE CloneIDs 132376-132391),
1456008-1456775, 1500552-1502855) NCI_CGAP_Kid5 pool 1:
LLAM 3338-3342, 3722-3723, 376-3778 (IMAGE CloneIDs
1323912-1325811, 1471368-1472903, 1492104-1493355)
NCI_CGAP_Lo19, pool 1: LLAM 357-3582, 3851-3854 (IMAGE
CloneIDs 1414920-1417991, 1520904-1522439, NCI_CGAP_GC4
pool 1: LLAM 316-3167, 3716-3720, 3733-3735 (IMAGE
CloneIDs 1450491, 1516-376, 146964-1470983, 1475592-1476743
) NCI_CGAP_DC2D pool 1: LLAM 2457-2459, 2758-2759,
1217928-1220615) NCI_CGAP_CO10 pool 1: LLAM 2644-2653,
2871-2872 (IMAGE CloneIDs 1057416-1061255, 114454-1145351)
Subtraction was performed as previously described
Subtraction: Two Abstractors To Farilitate Gene Discovery
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TAG_LIB=NCI_CGAP_LU5
TAG_TISSUE=lung
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                                                                                                                                                                                                                                                                                                                                                                                                                              34.4%; Score 396.4; DB 10; 99.7%; Pred. No. 9.3e-63;
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813 agctcgtgattggaaactcaccatcggcaggcagtggttcggtttaagagatggcattag 872
                                                                158 GCCCATCTGCACAGTGGGGAGCATGGAGGGATGGGTTTGGCCTGTGCTTCTGCTTATTCA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 987 gcccatctgcacagtggggagcatggagggatgggttttggcctgtgcttctgcttattca 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     927 acactttggcccgaaatagatccagtgctgagcaagcaatgtacaccggagcctcagtga 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 CATTACAGGGAGCCCAGTCTGGATGTGGACTTGGATGCCCTGTGGGTATCAGTTCTGCTG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 ACACTTTGGCCCGAAATAGATCCAGTGCTGAGCAAGCAATGTACACCGGAGCCTCAGTGA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 GTCCTTCAGCTCACGGAAGGGATGCTAGTCCGTGAAGGTGACCTCACAGTACTGGTTAAT 39
                                                                                                                                                                            / Match 32.5%; Score 374.4; DB 10; Length 376; Local Similarity 99.7%; Pred. No. 9.7e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 TAAACTTTATTGCTCACTGTCAAAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI832007 376 bp mRNA EST 21-DEC-1999 wy99a02.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410922 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 375.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11547-015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                        /note-"Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
sal1; Site_2: Not1; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
a 105 c 97 g 82 t
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/clone_lib="NCI_CGAP_Lyml2"
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/db_xref="taxon:9606"
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377 CAAAATCCCCTTCATACCCACCAGNATGTGTGCCCAGCCAGGCCTCCAGCACCCCCAAGTG 318
                               256 AGGGAGCCCAGTCTGGATGTGGACTTGGATGCCCTGTGGGTATCAGTTCTGCTGACACTT 197
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                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qx10a04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2000910 3', mRNA_sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 336.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -40UP from Gibco
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Insert Length: 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
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l (bases l to 525)
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                                                                                                                     Conservative
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Sall; Site_2: Not1; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
a 141 c 136 g 104 t 1 others
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="lymphoma, follicular mixed small and large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NCI_CGAP_Lym12"
                                                                                                            32.4%; score 372.8; DB 10; Length 525; 99.2%; Pred. No. 1.7e-58; ative 0; Mismatches 3; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          992 tctgcacagtggggagcatggagggatgggtttggcctgtgcttctgcttattcagtcct 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                932 ttggcccgaaatagatccagtgctgagcaatgtacaccggagcctcagtgagccca 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 CAGCTCGTGATTGGAAACTCACCATCGGCAGGCAGTGGTTCGGTTTAAGAGATGGCATTA 258
                           Local
    350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGCACAGTGGGGAGCATGGAGGGATGGGTTTGGCCTGTGCTTCTGCTTATTCAGTCCT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGGCCCGAAATAGATCCAGTGCTGAGCAAGCAATGTACACCGGAGCCTCAGTGAGCCCA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nlh.gov
Eco RI site shown at the beginning of the sequence.
Tissue procurement: Louis M. Staudt, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW404913 358 bp mRNA EST 16-FEB-2000 UI-HF-BLO-acn-h-03-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3559932 5', mRNA sequence.
                       similarity 99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 358)
                                                                                                                                71 a
    Conservative
                                                                                                            M. Staudt, Ph.D. Library preparations. ____,
Bonaldo, Ph.D. and M. Bento Soares, Ph.D. = 103 c 115 g 69 t
                                                                                                                                                              /lab_host="DH10B (LTI)"
/note="Vector: pT713-Pa; Site_1: Not1; Site_2: Eco RI;
/note="Vector: pT713-Pa; Site_1: Not1; Site_2: Eco RI;
Constructed from Size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
(1.5-2.5kb). Library preparation by Maria de Fatima
Donaldo Ph. D. Library preparation by Maria de Fatima
                                                                                                                                                                                                                                                                                                                  /clone_lib="NIH_MGC_37"
/tissue_type="lymph"
                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:3059932"
                                                                                                                                                                                                                                                                               /cell_type="germinal center B cells"
/cell_line="MGC85"
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
    0,
                    Score 349.4; DB 1
Pred. No. 3.5e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA
    Mismatches
                                    DB 10; Length 358;
  Indels
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Gaps
0;
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 TCCAGTTTCTGGGAAATATCAGACCATGGCCAGATTGACTCTATGGAGCAG 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328 tccagtttctgggaaatagcagaccatggccagattgactctatggagcag 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 ttctcccagctgcccgccgtgtggcagctctaccccgggaggaagtaccgagcagcggat 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 GTGCACTTGTGGCAGATGGCAGTGCATACCCGGGAGCTACTCTCCTCCGGCCAGATGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 gtgcacttgtggcagatggcagtgcatacccggggagctactctcctccggccagatgccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 ccctcgcgtagggaatgggccagggcctcccagggcagcagatatgaacccagcatcaca 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 TTCTCCCAGCTGCCCGCCGTGTGGCAGCTCTACCCCGGGAGGAAGTACCGAGCAGCGGAT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 CCCTCGCGTAGGGAATGGGCCAGGGCCTCCCAGGGCAGCAGATATGAACCCAGCATCACA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 atggcctccgaagcttctgtgcgtctaggggtgccccctggccgtctgtggatccagagg 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 CCTGGCATCTACGAAGATGAGGAGGGGAGAACCTGGGTGACTGTGGTCGTGCGGTTCAAT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 cctggcatctacgaagatgaggagggagaacctgggtgactgtggtcgtgcggttcaat 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 ATGGCCTCCGAAGCTTCTGTGCGTCTAGGGGTGCCCCCTGGCCGTCTGTGGATCCAGAGG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.qov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA_Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                            www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1077 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 338)
                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 135.
          ]. Double-stranded cDNA was ligated to Eco RI adaptors
                                                                                                                                                                                                                                                                                       /clone="IMAGE:1354688"
                                                                                                                                                                                                                /lab_host="DH10B"
                                                                                                                                                                                                                                    /tissue_type="germinal center B cell"
                                                                                                                                                                                                                                                           /clone_lib="NCI_CGAP_GCB1"
                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1000 gtggggagcatggagggatgggtttggcctgtgcttctggcttattcagtccttcagctca 1059
                                                                                                        source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            940 aaatagatccagtgctgagcaatgtacaccggagcctcagtgagcccatctgcaca 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 CCAGTCTGGATGTGGATGCCCTGTGGGTATCAGTTCTGCTGACACTTTGGCCCG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 GATTGGAAACTCACCATCGGCAGGCAGTGGTTCGGTTTAAGAGATGGCATTACAGGGAGC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 AAATAGATCCAGTGCTGAGCAAGCAATGTACACCGGAGCCTCAGTGAGCCCCATCTGCACA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wq64e08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2476070 3',
                                                                                                                           Insert Length: 384 Std Erro
Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                 CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                           Ph.D.
/clone="IMAGE:2476070"
/clone_lib="NCI_CGAP_GC6"
                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.8%;
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Pred. No. 6.9e-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        986 agcccatctgcacagtggggagcatggagggatgggtttgggcttgtgcttctgcttattc 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 GCATTAGAGGGAGCCCAGTCTGGATGTGGACTTGGATGCCCTGTGGGTATCAGTTCTGCT 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 TTAAACTTTATTGCTCACTGTCAAAAAA 1
                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 315)
                                             DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1751 Std Error: 0.00
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
AI434322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ti4ld01.xl NCI_CGAP_Lyml2 Homo sapiens cDNA clone IMAGE:2133025 3',
                                                                                                                                                                                                                                     Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
High quality sequence stop: 308.
Location/Qualifiers
                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11547-015
                                                                                                                                                                                                                                                                                     Tumor Gene Index
                                                                                                                                                                                                                                                                                                            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. " a 95 c 73 g 76 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; plasmid DNA from the normalized library NCI CGAP GC4 was prepared, and ss circles were made in vitro. Following HAP purification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315 bp
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AI250350/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     992 tetgeacagtggggagcatggagggatgggtttggcetgtgettetgcttattcagtect 1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               932 ttggcccgaaatagatccagtgctgagcaatgtacaccggagcctcagtgagccca 991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 TTTATTGCTCACTGTC 1
                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                  High quality sequence stop: 269.
                                                                                                                                                                                unknown
                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI250350 300 bp mRNA EST 21-DEC-1998 qx04c01.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2000352 3',
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
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                                                                                                                                                                                                                                                                                                                         (bases 1 to 300)
                                                                                                                                      primer: -40UP from Gibco
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                                                                                                                                                                                                                                                             Gene Index
                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Lym12"
                   /clone="IMAGE:2000352"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note "Organ: lymph node; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"

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                                                                                                 Location/Qualifiers
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/clone_lib="NCI_CGAP_Lym12"
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                                                                                                                                                                                                                                              (1997)
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                                                                                                                                                          Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 ATGTACACCGGAGCCTCAGTGAGCCCATCTGCACAGTGGGAGCATGGAGGGATGGGTTT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 GGCCTGTGCTTCTGCTTATTCAGTCCTTCAGCTCACGGAAGGGATGCTAGTCCGTGAAGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  965 atgtacaccggagcctcagtgagcccatctgcacagtggggagcatggagggatgggttt 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 AGTGGTTCGGTTTAAGAGATGGCATTAGAGGGAGCCCAGTCTGGATGTGGACTTGGATGC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     845 agtggttcggtttaagagatggcattagagggaagcccagtctggatgtggacttggatgc 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 TGACCTCACAGTACTGGTTAATTAAACTTTATTGCTCACTGTCCA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                     Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
                                                                                                                                                                                                                          401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887
                                         High quality sequence stop: 492.
Location/Qualifiers
1. .492
                                                                                                  Class: BAC ends
                                                                                                                                                                                                                                                                                      High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                               scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                       Seq primer: T7
                                                                                                                                                                                                                                                                                                                             Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                          99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ589625 492 bp DNA GSS UB-JUN-1999
HS_2132_Al_D12_T/C CIT Approved Human Genomic Sperm Library D Homo
sapiens_genomic clone Plate=2132 Col=23 Row-G, DNA sequence.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="lymphoma, follicular mixed small and large cell" \label{eq:cell}
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                                                                                                                                         row: G column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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BASE COUNT
ORIGIN
                                                                            QΥ
                                                                                                          Вþ
                                                                                                                                                             Дb
                                                      Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 22.8%; Score 262.8; DB 13; Length 492; Best Local Similarity 75.1%; Pred. No. 1.9e-38; Matches 396; Conservative 0; Mismatches 87; Indels 44;
                                                                                                                                                                                                                                                                 124 TCCCATGGCAGCATATGAACCTAGCATCACAGTGCACATGTGGTAGATGCCAGTGCAC 183
                                                                                                                                                                                                                                                                                                                                     175 tcccagggcagcagatatgaacccaggcatcacagtgcacttgtggcagatggcagtgcat 234
                                                                                                                          300 -- CCAGATCGTCTCCATGGAGCAGCTGGTCCTAACATATTGGCCGGCAAGGAATAACTGA 357
                                                                                                                                                                            355 ggccagattgactctatggagcagctggtcctaacatatcagccggagaggaaagactga 414
                                                                                                           358 ----CTCCTCTGGCCTCATGTCTCTCTCGGCCC 386
                                                                                                                                                                                                                                                                                                                                                                                                                              103 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B" a 148 c 124 g 112 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="plate=2132 Col=23 Row=G"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 87; Indels 44; Gaps
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Search completed: November 29, 2001, 05:49:45 Job time: 6331 sec